

Amendments to the Specification:

Please replace the paragraph beginning at page 16, line 18, with the following rewritten paragraph:

All five mutant proteins listed in Table 4 have the amino acid substitutions T117R and G188L, in combination with various substitutions at the remaining four positions. The fact that these two mutations are the optimal changes at their respective positions for reducing chain length specificity suggests that they are likely the primary determinants of the altered specificity in com2. The observation that several other mutants containing this pair of mutations have lower specific activity suggests that the combination of mutations at the remaining four randomized sites can also affect the specific activity of the mutants. This conservation suggests that the substitutions T117R and ~~G118L~~ G188L are responsible for the change in substrate specificity of the five mutants in Table 4. A mutant desaturase with the combination of T117R and ~~G118L~~ G188L substitutions is expected to have enhanced activity for one or more substrates with 16 or fewer carbons.

Please replace the paragraph beginning at page 32, line 28, with the following rewritten paragraph:

While the use of structure-guided (i.e., directed) mutagenesis of residues M114, L118, ~~P170-P179~~ and G188 was effective for the identification of seven mutants with substrate specificities of 16 or fewer carbon fatty acids, the method relied on the appropriate choice of target residues for mutagenesis. It is well documented that residues that affect substrate specificity fall into two broad classes, direct and indirect. Thus, random mutagenesis selection provides a bias-free method for the identification of changes that result in increased specificity for shorter acyl chains. Through random mutagenesis and selection of the present invention, five amino acid positions were identified, three at sites that were also targets for the structure-guided mutagenesis and two new sites, T117 and T181.